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; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17..(3768)
US-11-202-516-3

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DB:	12	Gaps: 0

US-09-493-480-7 (1-712) X US-11-202-516-3 (1-3768)

[illegible]

Dh	761	AGCGCATCTGTGAGCGTCACTCGCCGAGCCCTGAGTCACTCAACAACAGAGACGTTTGTAG	840
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Dh	841	TCGACGCCCATCCCGAGAGGCGCGGTATACATTCGCGCGAGCTGTGATGACCTGCTGCC	900
Oy	301	TyrAaMylTLeuSeArThaAPValGlySeCySerThLeuValCyseProGluAlaGln	320
Dh	901	ThACACTTACATAGTAAAGGATGATGTAATGCTGATGCTGCTGCTGCTGCTGCAACCA	960
Oy	321	GluValAlaThrAlaGluAaGlyGlyThrGlnAArgGlyGlySeSerTyProCyValAlaTy	340
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Oy	341	ValCyTyArgTyLeuGlyTMetGlyLysIleAlaMetGluValAlaArgAlaValThrSerAlaAn	360
Dh	1021	GTGTCTCATGATGTCTGGAGAGAGACCTTGAGAGAGGTGAGAGGAGGACGATACAGATGCA	1080
Oy	361	ILeGlnLysPheAlaGlyCyValLysValIlePheGlySerThLeuAlaPheLeuProGlySeC	380
Dh	1081	ATCCAGAGATCTTGTGCTGTGCAAGAGATCTTTGTGGAGACCTGTGCACTTCTCGAGAGAG	1140
Oy	381	PheAProTyAPAPProAlaSeSerArThAlaAProLeuGlnProGluInGlyGlnValPhe	400
Dh	1141	TTTGATGTGGGAGCCGACGCTCCAAACCTGCGCCCGCTCCGACAGAGAGCTCAAGATTT	1200
Oy	401	GluThyPLeuGlnGluLysIleThrTyTrLeuSerTyLLeuPheAlaThrAPAPProGlyPro	420
Dh	1201	GAGATCTGTGAGAGAGATACAGACAGGATACATCTGATGATGATATGTGGCGAGACCTGTGC	1260
Oy	421	AlaAspLeuSeArThPheAlaAspArgProHISArgGlyTyLLeuLysIleGlnGlyAla	440
Dh	1261	GACCTCAGCGCTCTTCCACACACCTGAGACGATATCCGCGGGAGCAAAATTTGTGACAGATGGCC	1320
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Oy	461	LeuGlySerGlyLeuAlaIleTrpIleHisAlaMetThrIleGluGlyProPheValIleGlyTyAla	480
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Oy	481	ProTyrArgGlnIleuPheAlaAspArgProHISArgLysIleGlyAlaAlaAlaArgPro	500
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Oy	501	GluAaPLeuCyValGlyGlyGlnTyLeuAlaCyGlyHisIleGlnIleGlyValAlaArgGlySeC	520
Dh	1501	GAGACACAGAGTGTGTGCGAGATCTGGCTGGCTGACAGAGCTGTGGCCCGAGAGGCACTGCG	1560
Oy	521	TrpArgIleArgProThGlnGlyGlyAlaAsnCySeSerArThPheLeuAlaGlyIleGlnGlyCyE	540
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Oy	541	ValGlnGlyCyValGlyValLeuGlnIlePheAProArgGlyTyValAlaMetAlaArgIleSeC	560
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Oy	561	LeuProCyHisIleAProLysCyArgIleProGlnAaGlyLysArgTyAlaThrCyPheGlyTyProLys	580
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Oy	581	AlaAPAPGlnCyValAlaCyValAlaIleTyTrTyAPAPProProPheCyValAlaAlaArgCyE	600
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Oy	621	GlyAlaCyGlnIleProCyAPProIleAlaMetCySerThIleSeSerTyValAlaAPAPLeuAPAPTyE	640
Dh	1861	GCGGCACTGACACCTTGTGCCCATCAATGTCAGACCGACCTGTGTGTAACTCTGGAATGAACAG	1920







TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2185 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: homo sapiens  
INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene, Fig. 8  
US-09-146-283-5

Alignment Scores:	
Pred. No.:	0
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Best Local Similarity:	100.0%
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Mismatches:	0
Indels:	0
Gaps:	0

US-09-493-480-7 (1-712) X US-09-146-283-3 (1-23851)

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Qy	21	AlaSerThrGlnValCysThrGlyThrAspMetLeuIleGluLeuProAlaSerProGlu	130
Db	71	GGACACACCGACAGGTGGACCGGACACACACACACACACACACACACACACACACAC	140
Qy	81	GlnGlyValLeuLeuIleAlaSerProGlnValAlaGlyArgTrpGlyValLeuLeuProGlnVal	160
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Db	121	ACCCACCTGGACACACCTCTCCGCGACCTCTCAACAGGCGTGGCGAGTGGCGAGAACCT	190
Qy	61	GluLeuThrGlyLeuLeuProThrAspAlaSerLeuAspSerPheLeuGlnAlaGlnAlaIle	80
Db	251	CAGGCGCTACCTGCTCATCTCCCTCAACCAACCAAGAGAGAGAGAGAGAGAGAGAGAG	310
Qy	81	GlnGlyValLeuLeuIleAlaSerProGlnValAlaGlyArgTrpGlyValLeuLeuProGlnVal	100
Db	371	GACCCGCTGACAAATACACCCCTGTGACAGGGGCTCCCGAGAGAGCTGGCGGAGACT	430
Qy	101	IleValArgGlyThrGlnLeuPheGlnIleAspAsnTrpAlaLeuAlaValLeuAspGlnGly	120
Db	311	ATTGTGCGACGACACCCGCTCTTGTGAGACACACACACACACACACACACACACACAC	370
Qy	121	AspProLeuAspAsnThrThrProValThrGlyAlaSerProGlnValIleAspTrpGlnIle	140
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Db	431	CACCTCGAAGGCTTCAACAAACACTTGGAAAGAGGGGGTCTGTATCCACCGAAGCCCCG	490
Qy	161	LeuCysTrpGlnIleAspThrIleLeuTrpValAspIlePheHisAlaValAspAsnGlnIleAla	180
Db	491	CTCTCTACACGACGACACATTTTGTGAGAGACACACTTCCACAGACACACACACACAC	550
Qy	181	LeuThrLeuIleLeuAspThrAlaAspGlySerAlaCysIleProCysSerProCysCysIle	200
Db	551	CTGACACGATAGACACACACCCGCTGTGGGCGCTGGACACCCCTGTCTCCGATGTGTAG	610
Qy	201	GlySerArgGlyTrpGlyValIleSerSerGlnIleAspCysGlnIleLeuThrAspThrValCys	220
Db	611	GGCTGCGCGCTGGGGGAGAGAGCTGTAGAGATGTGTACAGCTGACCGCACCATCTCTGT	670
Qy	221	AlaGlyGlyCysAlaArgCysValGlyProLeuProThrAspCysHisGlnGlnCys	240
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[illegible]

Fri Feb 17 09:07:52 2006

US-09-493-480-7.0119\_p2n.rml

Page 1

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Searched: 1303057 seqs, 888780828 residues

Wc: 1

Total number of hits satisfying chosen parameters: 2539977

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	653	91.7	3768	2	US-08-625-101-1
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11	653	91.7	4473	3	US-09-441-411-5
12	653	91.7	4530	2	US-08-229-515A-9
13	653	91.7	4530	2	US-08-645-865-9
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#### ALIGNMENTS

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Sequence 3, Application US/09146283  
Patent No. 5976546  
GENERAL INFORMATION:  
APPLICANT: Laus, Reiner  
INVENTOR: Laus, Reiner  
ATTORNEY: Ruesig, Curtis L.  
TITLE: IMMUNOSTIMULATORY COMPOSITIONS  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Ave. Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIA TYPE: floppy disk  
MEDIA SIZE: 5.25  
OPERATING SYSTEM: DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09146,283  
FILING DATE: 03-SEPT-1998  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Judge, Linda R. 42,702  
REGISTRATION NUMBER: 7636-0010.21  
REFERENCE/DOCNO NUMBER:  
TELEPHONE: 650-324-0880

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US-09-493-480-7 (1-712) x DQ047380 (1-3695)

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neuro/glioblastoma derived oncogene homolog (avian) (BRB2),
transcript variant 1, mRNA sequence.
EST
DQ04218.1 GI:66264091
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryotes; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
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1 (bases 1 to 762)
Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,H.,
Zhang,X., Zeng,G. and He,G. full-length human cDNAs directly from
chips: a library optimized for large and rare transcripts
unpublished (2005)
COMMENT
Contact: Kovacs, KF
High Throughput cDNA Cloning
Origene Technologies, Inc. ( www.origene.com )
6 Tate Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: cDNA@origene.com
This EST submission is part of an on-going human full-length
cloning project at Origene Technologies, Inc.
Please contact Origene for access.
Origene Technologies, Inc.
6 Tate Ct Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
Seq primer: PCMV5 Splice forward vector primer, Origene
Technologies Inc.
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                large inserted into mammalian expression vector. Random
                clones selected for mammalian expression verification of
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                Technologies"

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PA (RICE-) 1ST RICECHIE BIOL MOLECULANE ANGELETTI.  
PA  
XX Gallo P, Monaci P, Nuzzo M;  
X1  
XX WPI: 2005-123289/13.  
DR  
XX P-PSDB: ADM87401.  
XX  
PT New synthetic nucleic acid molecule encoding human epidermal growth  
PT factor 2 (HER2)/neu or HER2/CDTM protein, useful for preventing or  
PT treating HER2-associated cancer.  
XX  
XX  
PS Claim 7: SEQ ID NO 9; 62bp; English.  
PS  
XX The invention relates to a synthetic nucleic acid molecule which  
XX completely encodes a protein, (b) encoding a human HER2/CDTM  
XX complete sequence (HER2)/neu protein, (c) encoding a human HER2/CDTM  
XX protein, and (c) encoding a variant human HER2/neu or HER2/CDTM  
XX polypeptide. The sequence, vector, vaccine, composition, and methods are  
XX useful for preventing or treating HER2-associated cancer. The present  
XX sequence represents the human codon-optimized HER2/CDTM DNA.  
XX  
XX Sequence 2028 BP; 338 A; 802 C; 619 G; 269 T; 0 U; 0 Other;  
XX

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US-09-493-480-7 (1-712) X ADM87396 (1-2028)

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OY	61	GluThrTrpTrpLeuProGlyProGlyAsnLeuSerPheLeuGlnAspIleGlnIleVal	80
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OY	101	IleValIleArgIleThrGlyLeuLeuPheGlyAspAspTrpAlaLeuAlaValLeuAspAspGly	120
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OY	141	GlnLeuArgSerLeuTrpGlnIleLeuAlaArgIleGlyValaIleuIleGlnAspAspProGln	160
Db	421	CAGTGTCCGACGCTCAACGAGATCTCCAGAGAGGGCGGCGTCAACGCGACCCCGCAC	480
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[illegible]



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US-09-493-480-7 (1-712) x CS020247 (1-2028)

[illegible][illegible]

Fri Feb 17 09:07:52 2006

US-09-493-480-7.0119\_p2n.rge

Page 1

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 16, 2006, 14:00:33 / Search time 9196.63 Seconds

(without alignments)  
4400.801 Million cell updates/sec

Title: US-09-493-480-7

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Pred No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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ACCESSION	CS020247.1	GI:60220905			
VERSION	CS020247.1				
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE	1				
AUTHORS	Gallo, P.I., Monaci, P.I. and Nuzzo, M.I.				
TITLE	Synthetic gene encoding human epidermal growth factor 2/neu antigen				
JOURNAL	Patent: WO 200501527-A-9, 10-FEB-2005;				
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Fr1 Feb 17 09:07:51 2006

us-09-493-480-6.011g\_p2n.rnpbm

Page 2

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Query Match: 71.1% Indels:
DB: 6 Gaps:

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Ds	1081	ATCCGAGGATTTGGTGGTCTCAAGAGAGATCTTGGAGACCTGGACATCTGCACAGAGG	1140
Oy	381	PheAspGlyValProAlaSerAlaGlnHisAlaProLeuGlnProGlnIleuGlnValPhe	400
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Oy	401	GluHisIleuGlnGluHisIleHisGlyValLeuLeuValIleSerAlaTyrProAspSerLeuPro	420
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Ds	1261	GAGCTCAAGGCTCTCCAGAACCTCGAGAGATCCGGAGGAGAGATATCTCGACAGATGGGCG	1320
Oy	441	TyrSerIleuHisIleuGlnIleGlyLeuGlyIleIleSerTyrPheAsnValLeuAspSerLeuAlaGly	460
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; Sequence 8, Application US/09811122  
; Patent No. US20020001587A1  
; GENERAL INFORMATION:  
; APPLICANT: Sharon Erickson  
; APPLICANT: Ralph Schwall  
; APPLICANT: Mark Sliwowski





TELEFAX: 650-324-0960  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2385 base pairs  
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 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: homo sapiens  
 INDIVIDUAL ISOLATE: GM-CSF-HR-2 fusion gene; Fig. 8  
 US-09-146-283-3

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US-09-493-480-6 (1-919) x DQ047380 (1-3695)

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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.  
 REFERENCE  
 1 (bases 1 to 885)  
 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL  
 Unpublished (1999)  
 COMMENT  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaab@remail.nih.gov  
 Tissue Procurement: Kristi A. Eglund, Iva Pastan  
 cDNA Library Prepared by: The I.M.A.G.E. Consortium (LMU)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LMU at:  
 http://image.llnl.gov  
 Plate: LHM4285 row: 1 column: 17  
 High quality sequence stop: 717.

FEATURES  
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 Location/Qualifiers  
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 /lab\_host="EMBL10B"  
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 /note="Vector: pCMV-SPORT6; Site\_1: EcoRV; Site\_2: Not I;  
 subcloned with brain, liver, lung, kidney and muscle.  
 directionally cloned. Priming method: oligo-dT. Average  
 insert size: 1800 bp. Library amplification: 26,000 fold.  
 Kristi A. Eglund, James U. Vincent, Robert Strausberg,  
 Bunkook Lee & Iva Pastan.  
 Cancer genes and secreted proteins.  
 Manuscript submitted."

ORIGIN

Alignment Scores:  
 Pred. No.: 8.18e-251 Length: 885  
 Score: 261.00 Matches: 261  
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 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 28.4% Gaps: 0  
 DB: 6

US-09-493-480-6 (1-919) x CA455074 (1-885)



Fr1 Feb 17 09:07:51 2006

us-09-493-480-6.01tg\_p2n.rng

Page 2

PA (RICE-) 1ST RICECMB BIOL. MOLECOLAB ANGELETTI.  
XX  
XX Gallo P, Monaci P, Nuzzo M;  
PI  
PI WPI: 2005-123289/13.  
DR P-PSDB: A0M67401.  
XX  
XX  
XX New synthetic nucleic acid molecule encoding human epidermal growth factor 2 (HER2)/neu or HER2/CDTM protein, useful for preventing or treating HER2-associated cancer.  
XX  
XX  
XX Claim 7: SEQ ID NO 9; 62bp; English.  
XX  
XX The invention relates to a synthetic nucleic acid molecule which comprises a sequence of nucleotides: (a) encoding a human epidermal growth factor 2 (HER2)/neu protein; (b) encoding a human HER2/CDTM protein; and (c) encoding a vector vaccine composition, and methods are useful for preventing or treating HER2-associated cancer. The present sequence represents the human codon-optimized HER2/CDTM DNA.  
XX  
XX Sequence 2028 BP; 338 A; 802 C; 619 G; 269 T; 0 U; 0 Other;

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Best Local Similarity:	100.0%
Query Match:	71.1%
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Matches:	653
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-09-493-480-6 (1-919) x ADW87396 (1-2028)

[illegible]

OY	202	GLYSGRSTCYGTRFDLGGVLSSESGEGLVMPGSGVNSERLEATHVATGTHVAVG	220
DB	601	GGAGCCGCTCTGAGGGGAGAGAGACGAGAGACCTGACAGAGCTGACCCGACCCGTCG	660
OY	221	ALAAGLVAVYVALAAVGYVLSYEDGVLPOLVPRQTHVAPGYGCVGHSLEGLVGL	240
DB	661	GGCGGAGCGTCTGAGCCGCTGAGCCGCTGAGCCGCTGAGCCGCTGAGCCGCTGAGCCGCTG	720
OY	241	ALAALAVCYGTHRGLPRQVPHLSSESTAPGCVLEMLACVLEMLHSPHEANHS	260
DB	721	GGCGCGGCTGCAACCGGCCCCAGAGAGACCACTGGCTGCGCTGCACTCAACAC	780
OY	261	SEEGGLVLCYGVGLVLEMLHSECYPRQALALENVATHTYVASTHTVAPRTHPHEGLV	280
DB	781	AGCGGCACTCTGAGAGCTGACGCGCCCGCTGGAGACATCAACACCAACCTTGAC	840
OY	281	SEETHEPRQAMPRLQGLVATGTHVTHPHEGLVHSECVGLVATHVAPRQ	300
DB	841	AGCGAGCGGACCGGAGCGGCGCTGACCTTGCGCGAGCTGAGACCCGTCGCCC	900
OY	301	TYVASTHTVLESTHTHAPVAVGLVSECTGYTHLENVATVCPOLVLEMLHSPHEANHS	320
DB	901	TAAACACTCGGACCAACGACGAGGAGACGCTGACCCGCTGATGCGCCCTGCAACCAAC	960
OY	321	GLVAVATHVLAAGLVMPGSLVTHLVATGCVGGLVLYGCVSESTVPRQVVALAVG	340
DB	961	GAAGTACACCGGAGAGAGAGACGACCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG	1020
OY	1021	GTGCTCTACCGCTGGCGGCAVAGAGACCTGCGAGAGATGCGCGCGCTGACAGGCGAAC	1080
OY	361	ILSGNLVPHALADLVYALVLYGLVLEPHEDVSGSTLEMLHAPHEMLPRQUGSER	380
DB	1081	ATCCAGAGATGCGCGCTGCAAGAAATCTTGAGACCTGACCTCTCTGCGAGAGAC	1140
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DB	1141	TTGACAGGCGGACCGGCAACAGACCGCGCCCTGCTGACCGCGAGACGCTGAGAGTTC	1200
OY	401	GLVTHRLEMLVGLVGLVTHRGLTYVLEMLVTLSESGVATPRQVAPSESTLEMLPR	420
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DB	1321	TACAGCTGACCGGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTG	1380
OY	461	LEMLVSGRGLVLEMLHLEMLHLEMLHSPHEANHTVLAELVCPHEVATHTVATGLV	480
DB	1381	CTGGGCGAGCGCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	1440
OY	481	PRQTHAPRQGLVPHAPRQGLVPHAPRQGLVPHAPRQGLVPHAPRQGLVPHAPRQGLV	500
DB	1441	CCCTGCGAGCGGCTGCTGCGAGACCGGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCTG	1500
OY	501	GLVAPRQGLVAVATGLVATGLVLEMLHACVGHSLGGLVLEMLVATGLVATGLVATGLV	520
DB	1501	GAGAGACGAGCGTGGAGAGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	1560
OY	521	TRPGVLPRLQVPRQTHVATGLVATGLVATGLVATGLVATGLVATGLVATGLVATGLV	540
DB	1561	TGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	1620
OY	541	VATGLVATGLVATGLVATGLVATGLVATGLVATGLVATGLVATGLVATGLVATGLV	560
DB	1621	GTGAGAGAGAGCGCGTGGAGAGGCTGAGCGCGGCGGAGATGACGTAACGCGCGGCTG	1680
OY	561	LEMPRQVPHLSAPRQGLVATGLVATGLVATGLVATGLVATGLVATGLVATGLVATGLV	580



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Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	71.1%	Indels:	0
DB:	6	Gaps:	0

[illegible][illegible]

Fri Feb 17 09:07:51 2006

us-09-493-480-6.01ig\_p2n.rge

Page 1

GenCase version 5.1.7  
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OM protein - nucleic search, using frame\_p2n model

Run on: February 16, 2006, 14:00:33 / Search time 11870.4 Seconds  
(without alignments)  
400,801 Million cell updates/sec

Title: US-09-493-480-6

Perfect score: 319  
Sequence: 1 METAACRQGLALLPPGK.....TFKQTPFTHNPVYGLDVPV 919

Scoring table:

Xgapop 60.0, Xgapext 60.0  
Ygapop 60.0, Ygapext 60.0  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 588141 seqs, 2842172563 residues

1

Total number of hits satisfying chosen parameters: 11757827

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:  
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-LIST=45 -DOCLUT=200 -HRS=SCORES=quality -HRS=MIN=1 -HRS=MAX=100 -HRS=LCCL  
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-WARN TIMOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELTOP=6 -DELEXT=7

Database:

GenBank: 1: gb\_da: 2: gb\_in: 3: gb\_env: 4: gb\_om: 5: gb\_ov: 6: gb\_ov: 7: gb\_ov: 8: gb\_ov: 9: gb\_ov: 10: gb\_ov: 11: gb\_ov: 12: gb\_ov: 13: gb\_ov: 14: gb\_ov: 15: gb\_ov:

Prod. No. is the number of results predicted by change a score greater than or equal to the prod. No. being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match Length	DB ID	Description
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3	653	71.1	2385	AK082744

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# ALIGNMENTS

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VERSION	CS020247.1				
KEYWORDS					
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1 Gallo P.I., Monaci P.I. and Nuzio M.I.				
AUTHORS	Synthetic gene encoding human epidermal growth factor 2/neu antigen				
TITLE	and uses thereof				
JOURNAL	Patent: WO 2005012527-A-9 10-FEB-2005				
INSTRUMENT	Istituto di Ricerche di Biologia Molecolare P. Angeletti S.P.A.				
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